Amendments to Claims:

This listing of claims will replace all prior versions and listings of claims in the instant application:

Listing of Claims:

1. (Currently Amended). ~~Method~~ A method for *in vitro* detection of acute generalized inflammatory conditions (SIRS), ~~characterized in that it comprises the following steps:~~ comprising

a) ~~Isolation of~~ isolating sample RNA from a sample of a mammal;

b) ~~Labelling~~ labeling of the sample RNA and/or at least one DNA being a gene or gene fragment specific for SIRS, with a detectable label;

c) ~~Contacting~~ contacting the sample RNA with the DNA under hybridization conditions;

d) ~~Contacting~~ contacting the sample RNA representing a control for non-pathologic conditions, with at least one DNA, under hybridization conditions, whereby the DNA is a gene or gene fragment specific for SIRS;

e) ~~Quantitative~~ quantitating detection of the label signals of the hybridized sample RNA and control RNA;

f) ~~Comparing~~ comparing ~~the~~ quantitative data of the label signals in order to determine whether the genes or gene fragments specific for SIRS are more expressed in the sample than in the control, or less.

2. (Currently Amended). ~~Method~~ A method for *in vitro* detection of sepsis and/or sepsis-like conditions, said method comprising ~~characterized in that it comprises the following steps:~~

g) ~~Isolation of~~ isolating ~~of~~ sample RNA from a sample of a mammal;

h) ~~Labelling~~ labeling of the sample RNA and/or at least one DNA being a gene or gene fragment specific for sepsis, with a detectable label[[.]] ;

i) ~~Contacting~~ contacting the sample RNA with the DNA under hybridization conditions;

j) ~~Contacting~~ contacting the sample RNA representing a control for non-pathologic conditions, with at least one DNA, under hybridization conditions, whereby the DNA is a gene or gene fragment specific for sepsis and/or sepsis-like conditions;

k) ~~Quantitative~~ quantitating detection of the label signals of the hybridized sample RNA and control RNA;

l) ~~Comparing~~ comparing ~~the~~ quantitative data of the label signals in order to determine whether the genes or gene fragments specific for sepsis and/or sepsis-like conditions are more expressed in the sample than in the control, or less.

3. (Currently Amended). ~~Method~~ A method for *in vitro* detection of severe sepsis, said method comprising ~~characterized in that it comprises the following steps~~:

m) ~~Isolation of~~ isolating sample RNA from a sample of a mammal;

n) ~~Labelling~~ labeling of the sample RNA and/or at least one DNA being a gene or gene fragment specific for severe sepsis, with a detectable label.

o) ~~Contacting~~ contacting the sample RNA with the DNA under hybridization conditions;

p) ~~Contacting~~ contacting sample RNA representing a control for non-pathologic conditions, with at least one DNA, under hybridization conditions, whereby the DNA is a gene or gene fragment specific for severe sepsis;

q) ~~Quantitative~~ quantitating the detection of the label signals of the hybridized sample RNA and control RNA;

r) ~~Comparing~~ comparing the quantitative data of the label signals in order to determine whether the genes or gene fragments specific for severe sepsis are more expressed in the sample than in the control, or less.

4. (Currently Amended). ~~Method~~ The method according to any one of claims 1 to 3, ~~characterized in that the control~~ wherein RNA is hybridized with the DNA before the measurement of the sample RNA and the label signals of the control RNA/DNA-complex is gathered and, ~~if necessary,~~ recorded in ~~form of~~ a calibration curve or table.

5. (Currently Amended). ~~Method~~ The method according to ~~one of claims 1 to~~ claim 4, ~~characterized in that~~ wherein unchanged genes from sample and/or control RNA are used as reference genes for the quantification.

6. (Currently Amended). ~~Method~~ The method according to ~~one of claims 1 to~~ claim 5, ~~characterized in that~~ wherein mRNA is used as sample RNA.

7. (Currently Amended). ~~Method~~ The method according to ~~one of claims 1 to~~ claim 6, ~~characterized in that~~ wherein the DNA is arranged, particularly immobilized, on predetermined areas on a carrier in the form of a microarray.

8. (Currently Amended). ~~Method~~ The method according to ~~one of claims 1 to~~ claim 7, ~~characterized in that~~ wherein the method for early detection by means of differential diagnostics, for control of the clinical and therapeutic progress, for the individual risk evaluation in patients, for the evaluation whether the patient will respond to a specific treatment, as well as for post mortem diagnosis of SIRS and/or sepsis and/or severe sepsis and/or systemic infections and/or septic conditions and/or infections.

9. (Currently Amended). ~~Method~~ The method according to ~~one of claims 1 to~~ claim 8, ~~characterized in that~~ wherein the sample is selected from the following group: body fluids, in particular blood, liquor, urine, ascitic fluid, seminal fluid, saliva, puncture fluid, cell content, or a mixture thereof.

10. (Currently Amended). ~~Method~~ The method according to ~~one of claims 1 to~~ claim 9, ~~characterized in that~~ wherein cell samples are subjected a lytic treatment, if necessary, in order to free their cell contents.

11. (Currently Amended). ~~Method~~ The method according to ~~one of claims 1 to~~ claim 10, ~~characterized in that~~ wherein the mammal is a human.

12. (Currently Amended). ~~Method~~ The method according to any one of claims 1 ~~or 4 to~~ or 11, ~~characterized in that~~ wherein the gene or gene segment specific for SIRS is selected from the group consisting of SEQUENCE ID No. III.1 to SEQUENCE ID No. III.4168, as well as gene fragments thereof with between about 5-2000 ~~or more, preferably 20-200, more preferably 20-80~~ nucleotides.

13. (Currently Amended). ~~Method~~ The method according to any one of claims 2, ~~or~~ 4 ~~to~~ or 11, ~~characterized in that~~ wherein the gene or gene segment specific for sepsis and/or sepsis-like conditions is selected from the group consisting of SEQUENCE ID No. I.1

to SEQUENCE ID No. I.6242, as well as gene fragments thereof with between about 5-2000 ~~or more, preferably 20-200, more preferably 20-80~~ nucleotides.

14. (Currently Amended). ~~Method~~ The method according to any one of claims 3, ~~or~~ 4 ~~to~~ or 11, ~~characterized in that~~ wherein the gene or gene segment specific for severe sepsis is selected from the group consisting of SEQUENCE ID No. II.1 to SEQUENCE ID No. II.130, as well as gene fragments thereof with between about 5-2000 ~~or more, preferably 20-200, more preferably 20-80~~ nucleotides.

15. (Currently Amended). ~~Method~~ The method according to ~~one of claims 1 to~~ claim 14, ~~characterized in that~~ wherein at least 2 to 100 different cDNAs are used.

16. (Currently Amended). ~~Method~~ The method according to ~~one of claims 1 to~~ claim 15, ~~characterized in that~~ wherein at least 200 different cDNAs are used.

17. (Currently Amended). ~~Method~~ The method according to ~~one of claims 1 to~~ claim 16, ~~characterized in that~~ wherein at least 200 to 500 different cDNAs are used.

18. (Currently Amended). ~~Method~~ The method according to ~~one of claims 1 to~~ claim 17, ~~characterized in that~~ wherein at least 500 to 1000 different cDNAs are used.

19. (Currently Amended). ~~Method~~ The method according to ~~one of claims 1 to~~ claim 18, ~~characterized in that~~ wherein at least 1000 to 2000 different cDNAs are used.

20. (Currently Amended). ~~Method~~ The method according to ~~one of claims 1 to~~ claim 19, ~~characterized in that~~ wherein the cDNA of the genes listed in claims 12, 13 und 14 is replaced by synthetic analoga as well as peptidonucleic acids.

21. (Currently Amended). ~~Method~~ The method according to claim 20, ~~characterized in that~~ wherein the synthetic analoga of the listed genes comprise 5-100, in particular approximately 70, base pairs.

22. (Currently Amended). ~~Method~~ The method according to ~~one of claims 1 to~~ claim 21, ~~characterized in that~~ wherein a radioactive label, in particular ^{32}P, ^{14}C, ^{125}I, ^{155}Ep, ^{33}P or ^{3}H is used as detectable label.

23. (Currently Amended). ~~Method~~ The method according to ~~one of claims 1 to~~ claim 22, ~~characterized in that~~ wherein a non-radioactive label is used as detectable label, in particular a color- or fluorescence label, an enzyme label or immune label, and/or quantum dots or an electrically measurable signal, in particular the change in potential, and/or conductivity and/or capacity by hybridizations.

24. (Currently Amended). ~~Method~~ The method according to ~~one of claims 1 to~~ claim 23, ~~characterized in that~~ wherein the sample RNA and control RNA bear the same label.

25. (Currently Amended). ~~Method~~ The method according to ~~one of claims 1 to~~ claim 24, ~~characterized in that~~ wherein the sample RNA and control RNA bear different labels.

26. (Currently Amended). ~~Method~~ The method according to ~~one of claims 1 to~~ claim 25, ~~characterized in that~~ wherein the immobilized probes bear a label.

27. (Currently Amended). ~~Method~~ The method according to ~~one of claims 1 to~~ claim 26, ~~characterized in that~~ wherein the cDNA probes are immobilized on glass or plastics.

28. (Currently Amended). ~~Method~~ The method according to ~~one of claims 1 to~~ claim 27, ~~characterized in that~~ wherein the individual cDNA molecules are immobilized on the carrier material by means of a covalent binding.

29. (Currently Amended). ~~Method~~ The method according to ~~one of claims 1 to~~ claim 28, ~~characterized in that~~ wherein the individual cDNA molecules are immobilized onto the carrier material by means of adsorption, in particular by means of electrostatic and/or dipole-dipole and/or hydrophobic interactions and/or hydrogen bridges.

30. (Currently Amended). ~~Method~~ A method for *in vitro* detection of SIRS, ~~characterized in that it comprises the following steps~~ comprising:

a) ~~Isolation of~~ isolating sample peptides from a sample of a mammal;

b) ~~Labelling~~ labeling of the sample peptides with a detectable label;

c) ~~Contacting~~ contacting the labelled sample peptides with at least one antibody or its binding fragment, whereby the antibody binds a peptide or peptide fragment specific for SIRS;

d) ~~Contacting~~ contacting the labelled control peptides originating from healthy subjects, with at least one antibody or its binding fragment immobilized on a carrier in form of a microarray, whereby the antibody binds a peptide or peptide fragment specific for SIRS;

e) ~~Quantitative~~ quantitating detection of the label signals of the sample peptides and the control peptides;

f) ~~Comparing~~ comparing ~~the~~ quantitative data of the label signals in order determine whether the genes or gene fragments specific for SIRS are more expressed in the sample than in the control, or less.

31. (Currently Amended). ~~Method~~ A method for *in vitro* detection of sepsis and/or sepsis-like conditions, ~~characterized in that it comprises the following steps~~ comprising:

g) ~~Isolation of~~ isolating sample peptides from a sample of a mammal;

h) ~~Labelling~~ labeling of the sample peptides with a detectable label;

i) ~~Contacting~~ contacting the labelled sample peptides with at least one antibody or its binding fragment, whereby the antibody binds a peptide or peptide fragment specific for sepsis and/or sepsis-like conditions;

j) ~~Contacting~~ contacting the labelled control peptides stemming from healthy subjects, with at least one antibody or its binding fragment immobilized on a carrier in form of a microarray, whereby the antibody binds a peptide or peptide fragment specific for sepsis and/or sepsis-like conditions;

k) ~~Quantitative~~ quantitating detection of the label signals of the sample peptides and the control peptides;

l) ~~Comparing~~ comparing ~~the~~ quantitative data of the label signals in order to be able to determine whether the genes or gene fragments specific for sepsis and/or sepsis-like conditions are more expressed in the sample than in the control, or less.

32. (Currently Amended). ~~Method~~ A method for *in vitro* detection of severe sepsis, ~~characterized in that it comprises the following steps~~ comprising:

m) ~~Isolation of~~ isolating sample peptides from a sample of a mammal;

n) ~~Labelling~~ labeling of the sample peptides with a detectable label;

o) ~~Contacting~~ contacting the labelled sample peptides with at least one antibody or its binding fragment, whereby the antibody binds a peptide or peptide fragment specific for severe sepsis;

p) ~~Contacting~~ contacting the labelled control peptides originating from healthy subjects, with at least one antibody or its binding fragment immobilized on a carrier in form of a microarray, whereby the antibody binds a peptide or peptide fragment specific for severe sepsis;

q) ~~Quantitative~~ quantitating detection of the label signals of the sample peptides and the control peptides;

r) ~~Comparing~~ comparing ~~the~~ quantitative data of the label signals in order to determine whether the genes or gene fragments specific for severe sepsis are more expressed in the sample than in the control, or less.

33. (Currently Amended). ~~Method~~ The method according to ~~one of claims 30 to~~ claim 32, characterized in that the antibody is immobilized on an array in form of a microarray.

34. (Currently Amended). ~~Method~~ The method according to ~~one of claims 30 to~~ claim 33, ~~characterized in that~~ wherein said method is an ~~it is formed as~~ immunoassay.

35. (Currently Amended). ~~Method~~ The method according to ~~one of claims 30 to~~ claim 34, ~~characterized in that~~ wherein the method is used for early detection by means of differential diagnostics, for control of the clinic and therapeutic progress, for risk evaluation for patients as well as for post mortem diagnosis of SIRS and/or sepsis and/or severe sepsis and/or systemic infections and/or septic conditions and/or infections.

36. (Currently Amended). ~~Method~~ The method according to ~~one of claims 30 to~~ claim 35, ~~characterized in that~~ wherein the sample is selected from the following group: body fluids, in particular blood, liquor, urine, ascitic fluid, seminal fluid, saliva, puncture fluid, cell content, or a mixture thereof.

37. (Currently Amended). ~~Method~~ The method according to ~~one of claims 30 to~~ claim 36, ~~characterized in that~~ wherein cell samples are subjected a lytic treatment, if necessary, in order to free their cell contents.

38. (Currently Amended). ~~Method~~ The method according to ~~one of claims 30 to~~ claim 37, ~~characterized in that~~ wherein the mammal is a human.

39. (Currently Amended). ~~Method~~ The method according to any one of claims 30, 33, ~~to~~ or 38, ~~characterized in that~~ wherein the peptide specific for SIRS is an expression product of a gene or gene fragment selected from the group consisting of SEQUENCE ID No. III.1 to SEQUENCE ID No. III.4168, as well as gene fragments thereof with about 5-2000 nucleotides or more~~, preferably 20-200, more preferable 20-80 nucleotides~~.

40. (Currently Amended). ~~Method~~ The method according to any one of claims 31,-33, ~~to~~ or 38, ~~characterized in that~~ wherein the peptide specific for sepsis and/or sepsis-like conditions is an expression product of a gene or gene fragment selected from the group consisting of SEQUENCE ID No. I.1 to SEQUENCE ID No. I.6242, as well as gene fragments thereof with about 5-2000 nucleotides or more~~, preferably 20-200, more preferable 20-80 nucleotides~~.

41. (Currently Amended). ~~Method~~ The method according to any one of claims 32, 33, ~~to~~ or 38, ~~characterized in that~~ wherein the peptide specific for severe sepsis is an expression product of a gene or gene fragment selected from the group consisting of SEQUENCE ID No. II.1 to SEQUENCE ID No. II.130, as well as gene fragments thereof with about 5-2000 nucleotides or more~~, preferably 20-200, more preferable 20-80 nucleotides.~~

42. (Currently Amended). ~~Method~~ The method according to ~~one of claims 30 to~~ claim 41, ~~characterized in that~~ wherein at least 2 to 100 different peptides are used.

43. (Currently Amended). ~~Method~~ The method according to ~~one of claims 30 to~~ claim 42, ~~characterized in that~~ wherein at least 200 different peptides are used.

44. (Currently Amended). ~~Method~~ The method according to ~~one of claims 30 to~~ claim 43, ~~characterized in that~~ wherein at least 200 to 500 different peptides are used.

45. (Currently Amended). ~~Method~~ The method according to ~~one of claims 30 to~~ claim 44, ~~characterized in that~~ wherein at least 500 to 1000 different peptides are used.

46. (Currently Amended). ~~Method~~ The method according to ~~one of claims 30 to~~ claim 45, ~~characterized in that~~ wherein at least 1000 to 2000 different peptides are used.

47. (Currently Amended). ~~Method~~ The method according to ~~one of claims 30 to~~ claim 46, ~~characterized in that~~ wherein a radioactive label, in particular ^{32}P, ^{14}C, ^{125}I, ^{155}Ep, ^{33}P or ^{3}H is used as detectable label.

48. (Currently Amended). ~~Method~~ The method according to ~~one of claims 30 to~~ claim 47, ~~characterized in that~~ wherein a non-radioactive label is used as detectable label, in particular a color- or fluorescence label, an enzyme label or immune label, and/or quantum dots or an electrically measurable signal, in particular the change in potential, and/or conductivity and/or capacity by hybridizations.

49. (Currently Amended). ~~Method~~ The method according to ~~one of claims 30 to~~ claim 48, ~~characterized in that~~ wherein the sample peptides and control peptides bear the same label.

50. (Currently Amended). ~~Method~~ The method according to ~~one of claims 30 to~~ claim 49, ~~characterized in that~~ wherein the sample peptides and control peptides bear different labels.

51. (Currently Amended). ~~Method~~ The method according to ~~one of claims 30 to~~ claim 50, ~~characterized in that~~ wherein the probes used are peptides to which labelled antibodies are bound, which cause a change of signal of the labelled antibodies by change of conformation when binding to the sample peptides.

52. (Currently Amended). ~~Method~~ The method according to ~~one of claims 30 to~~ claim 51, ~~characterized in that~~ wherein the peptide probes are immobilized on glass or plastics.

53. (Currently Amended). ~~Method~~ The method according to ~~one of claims 30 to~~ claim 52, ~~characterized in that~~ wherein the individual peptide molecules are immobilized onto the carrier material by means of a covalent binding.

54. (Currently Amended). ~~Method~~ The method according to ~~one of claims 30 to~~ claim 53, ~~characterized in that~~ wherein the individual peptide molecules are immobilized on the carrier material by means of adsorption, in particular by means of electrostatic and/or dipole-dipole and/or hydrophobic interactions and/or hydrogen bridges.

55. (Currently Amended). ~~Method~~ The method according to ~~one of claims 30 to~~ claim 54, ~~characterized in that~~ wherein the individual peptide molecules are detected by means of monoclonal antibodies or their binding fragments.

56. (Currently Amended). ~~Method~~ The method according to ~~one of claims 30 to~~ claim 55, ~~characterized in that~~ wherein the determination of individual peptides by means of immunoassay or precipitation assay is carried out using monoclonal antibodies.

57. (Original). Use of recombinantly or synthetically produced SIRS-specific nucleic acid sequences, partial sequences or protein-/peptide-sequences derived thereof, individually or as partial quantities as calibrator in SIRS-assays and/or to evaluate the effects and toxicity when screening for active agents and/or for the preparation of therapeutics as well as of substances and compounds that are designed to act as therapeutics, for the prevention and treatment of SIRS.

58. (Original). Use of recombinantly or synthetically produced sepsis-specific and/or sepsis-like conditions-specific nucleic acid sequences, partial sequences or protein-/peptide-sequences derived thereof, individually or as partial quantities as calibrator in sepsis assays and/or to evaluate the effects and toxicity when screening for active agents and/or for the preparation of therapeutics as well as of substances and compounds that are designed to act as therapeutics, for the prevention and treatment of sepsis, sepsis-like systemic inflammatory conditions and sepsis-like systemic infections.

59. (Original). Use of recombinantly or synthetically produced severe sepsis-specific nucleic acid sequences, partial sequences or protein-/peptide-sequences derived thereof, individually or as partial quantities as calibrator in sepsis-assays and/or to evaluate the effects and toxicity when screening for active agents and/or for the preparation of therapeutics as well as of substances and compounds that are designed to act as therapeutics, for the prevention and treatment of severe sepsis.